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First record of *Furipterus horrens* (Cuvier, 1828) (Chiroptera, Furipteridae) in the Ecuadorian Andes

Isabel Warren[1,2], Laura Simba[3,4], Jorge Brito[4]

1 *Reserva: The Youth Land Trust, Washington D.C., USA*
2 *Fundación EcoMinga, Quito, Pichincha, Ecuador*
3 *Facultad de Ciencias Biológicas, Universidad Central del Ecuador, Quito, Pichincha, Ecuador*
4 *División de Mastozoología, Instituto Nacional de Biodiversidad (INABIO), Quito, Pichincha, Ecuador*

Corresponding author: *Isabel Warren (warren.isabel@gmail.com)*

Abstract. We present the first Ecuadorian records of *Furipterus horrens* (Cuvier, 1828) from outside the Amazon Rainforest. Our specimens, collected in the Río Manduriacu Reserve, Imbabura Province, is the first record of any individual from the family Furipteridae in the Ecuadorian Andes. The genetic divergences observed with cyt-b and COI markers (10–15%) support previous studies that *F. horrens* represents a species complex and that the western Ecuador population may represent an undescribed species. This represents a significant increase in the potential habitat for this species and highlights the need for increased research into tropical Andean bat taxonomy.

Key words. COI, cytochrome b, mist-netting, Neotropical forest, thumbless bat, tropical Andes

Warren I, Simba L, Brito J (2025) First record of *Furipterus horrens* (Cuvier, 1828) (Chiroptera, Furipteridae) in the Ecuadorian Andes. Check List 21 (2): 451–456. https://doi.org/10.15560/21.2.451

INTRODUCTION

Chiroptera is the second largest order of mammals, containing over 1,474 extant species, almost 23% of all described mammals (Voigt and Kingston 2016; Mammal Diversity Database 2024). This evolutionary success is reflected in their geographic range, with bats occurring on all continents except Antarctica (Mickleburgh et al. 2002). The extent of this taxonomic diversity is best shown within the Neotropics (Patterson and Pascual 1968), with South America containing nine of the 14 described families of Yangochiroptera (Gardner 2008; Mammal Diversity Database 2024).

The Furipteridae is one of the smallest families of Yangochiroptera, containing only two described species: *Furipterus horrens* (Cuvier, 1828) and *Amorphochilus schnablii* Peters, 1877 (Gardner 2008). Characterized by their thumbless appearance, these bats have a rudimentary, non-functional first digit, which is almost entirely covered by the propatagium (Albuja 1999; Tirira 2017). Endemic to the Neotropics, this family of bats is found throughout South and Central America (Emmons 1990; Gardner 2008; Alfaro-Lara et al. 2018). Ecuador, along with Peru, is home to both species, with *A. schnablii* occupying the dry forests on the west coast (Ibáñez 1986; Gardner 2008), while *F. horrens* typically inhabits the Amazon (Albuja 1999; Reid et al. 2000; Tirira 2017).

However, despite being widespread across the continent, relatively little is known about the natural history and population health of these bats. They are rarely caught in mist nets and, as such, specimens and data are scarce (Albuja 1999; Portella et al. 2017). We present the first records of *F. horrens*, which was previously thought to be confined solely to the Amazonian region of Eastern Ecuador, from the western slopes of the Andes.

METHODS

Collection and study of specimens. Located at the meeting point of the tropical Andes and Chocó biodiversity hotspots (Myers et al. 2000), the Río Manduriacu Reserve (RMR) is a 966 ha privately protected area managed by Fundación EcoMinga. The reserve has received local conservation recognition within the province as an "area of conservation and sustainable use in the northwest of Imbabura" (ACUSMIT). Surveying was conducted in the RMR during September of 2024 at three locations along the Manduriacu Grande

OPEN ACCESS

Academic editor: Roberto Leonan Novaes
Received: 14 February 2025
Accepted: 5 April 2025
Published: 11 April 2025

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River. Mist nets were used to capture bats over small streams and creeks between 18h00 and 00h00 on two consecutive nights at each site. Following extraction of each individual from the nets, standard morphological measurements were taken: (1) body mass; (2) forearm length; (3) head and body length; (4) tibia length; (5) tail length; (6) ear length.

Over the course of six nights of surveying, we captured two individuals of *Furipterus horrens*. Both individuals were captured on the same night at different nets located within the same site. One of the two individuals captured was collected as a specimen and preserved in 96% ethanol. This voucher specimen was deposited in the Instituto Nacional de Biodiversidad's mastozoological collection (MECN). All research was conducted under permits no. MAATE-ARSFG-2023-0145 and authorization of access to genetic resources no. MAATE-DBI-CM-2023-0334, both issued by the Ministerio del Ambiente Agua y Transición Ecológica del Ecuador. All bats were handled in accordance with the American Society of Mammalogists' guidelines for the use of wild animals in research (Sikes et al. 2016).

DNA extraction, sequence generation and assembly. DNA was extracted from liver tissue using the GeneJET Genomic DNA Purification Kit (K0722). The mitochondrial cytochrome b (cyt-b) gene was amplified through Polymerase Chain Reaction (PCR) with the forward primer MVZ05 and the reverse primer MVZ16 (Smith and Patton 1993), along with the GoTaq Green Master Mix 2X kit. The PCR protocol included an initial denaturation step at 95 °C for 2 min, followed by 35 cycles of denaturation at 95 °C for 30 s, annealing at 45 °C for 30 s, and extension at 72 °C for 80 s, concluding with a final extension at 72 °C for 5 min. Cyt-b sequencing was carried out using a MinION mk1c with Flongle Flow Cells release 10.4.1 and the Rapid Barcoding Kit 96 (SQK-RBK114.96), following standard operating procedures. Base calling was performed using Dorado version high accuracy model v. 4.3.0. The resulting fastq files were quality filtered at a Q score threshold of 9, and consensus sequences were generated using NGSpecies ID v. 0.3.0 (Sahlin et al. 2021).

Phylogenetics analyses. Species sequences within *Furipterus* were described by Davalos (2005) and Molina et al. (2024) for the cyt-b marker, Clare et al. (2007, 2011), Duda et al. (2012), Borisenko et al. (2008) for the COI marker, and outgroup (Pavan et al. 2013) were retrieved from NCBI's GenBank (Appendix Table A1). The sequence alignment was performed using the MAFFT algorithm in Mesquite v. 3.81 (Maddison and Maddison 2023). Maximum-likelihood (ML) trees were generated in MEGA v. 12 (Kumar et al. 2024) for both markers using the Kimura 2-parameter model (Kimura 1980), and the trees with the highest log-likelihood values are shown. The generated ML trees were manually rooted by segregating the outgroup branch in MEGA v. 12 (Kumar et al. 2024), which was also used to calculate pairwise genetic distances by Kimura 2-parameter model (Kimura 1980). Sequences generated for this research are available for other researchers in GenBank (accession numbers PV147227 (COI) and PV147124 (Cyt b).

RESULTS

***Furipterus horrens* (Cuvier, 1828)**
Figures 1, 2

New records (Figure 3). ECUADOR — Imbabura • Cantón Cotacachi, Reserva Río Manduriacu; 00.3031°N, 078.8578°W; 1145 m elev; 17.VI.2024; Warren I. leg.; 1 ♀ in ethanol, MECN8160. • Same locality and date; Warren I. obs.; 1 ♂, not collected.

Identification. *Furipterus horrens* is a small bat, weighing ca. 3 g, characterized primarily by its rudimentary thumbs, lacking any nail, and almost fully encased in the propatagium (Tirira 2017), a structure that is seen clearly in our specimen (Figure 1A). *Furipterus horrens* has a well-developed caudal membrane, with the tail extending just past the middle of the uropatagium (Figure 1B, C). The uropatagium of *F. horrens* also has characteristic patterning of lines perpendicular to the tail. Standard morphological measurements taken of the specimen are all consistent with those previously reported in the literature (Table 1). *Furipterus horrens* can be distinguished from *Amorphochilus schnablii*, the other "thumbless" bat species by the wart-like growths on its chin (Figure 1D–F).

Phylogeny. The 1,140-bp-long cyt-b sequence corresponding to MECN 8160 (GenBank accession no. PV147124) was part of a multiple sequence alignment (MSA) composed of four full-length DNA sequences. The samples from Ecuador (Manduriacu and Yasuní) form a well-supported clade together with those from Brazil (Carajás and Canaã dos Carajás) (Figure 2A). The genetic distance between individuals from Ecuador (AY621004 and MECN8160) and those from Brazil (NC048476 and MK033190) is 15%, as well as that observed between individuals from Ecuador. On the other hand, the distance between the individuals from Brazil (NC048476 and MK033190) and the individual from Yasuní, Ecuador (AY621004) is 10.32%, while with the individual from the Río Manduriacu Reserve (MECN8160) it is 13.83%.

The 657 bp long COI sequence corresponding to MECN 8160 (GenBank accession no. PV147227) was part of a multiple sequence alignment (MSA) composed of seven partial DNA sequences. The samples from

Figure 1. *Furipterus horrens* from Río Manduriacu Reserve, Imbabura, Ecuador. **A.** Rudimentary thumb, ventral view, ♀. **B.** Caudal membrane, dorsal view, ♀. **C.** Body, dorsal view, ♂. **D.** Face, ventral view, ♀. **E.** Face, front view, ♂. **F.** Face, side view, ♂.

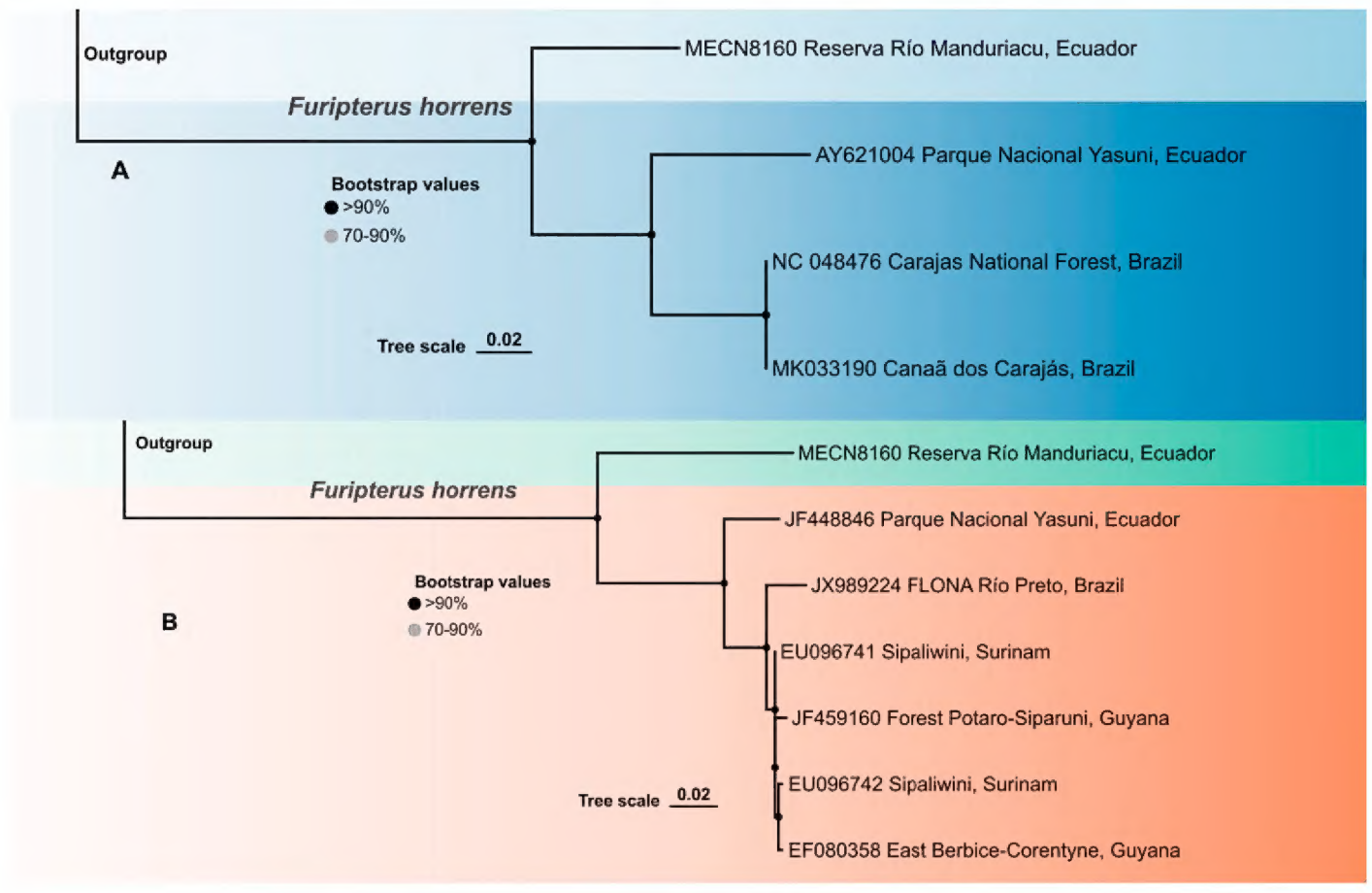

Figure 2. Phylogenies of *Furipterus horrens*, including the specimen from Rio Manduriacu Reserve, Imbabura, Ecuador (MECN 8160), based on the cytochrome b gene (**A**) and the cytochrome c oxidase subunit I gene (**B**).

Ecuador (Manduriacu and Yasuni) form a well-supported clade together with the one from Brazil (FLONA Rio Preto) (Figure 2B). The genetic distance between individuals from Ecuador (JF448846 and MECN8160) is 15.74%, while between Ecuador (JF448846) and Brazil (JX989224) is 5.75%. On the other hand, the genetic distance between individuals from Suriname (EU096742 and EU096741) is less than 1%, suggesting a high genetic similarity, as well as between individuals from Suriname and Guyana (JF459160). Finally, the individual from FLONA Rio Preto, Brazil (JX989224) shows a genetic distance of 15.9% with MECN8160.

Table 1. Comparative measurements of *Furipterus horrens* from Tirira (2017) and the two individuals captured in Imbabura Province, Ecuador.

Attribute	MECN 8160 (♀)	Released individual (♂)	(Tirira 2017)
Body mass (g)	3.9	3.7	2.4–4.0
Head and body length (mm)	33.7	34.0	32.0–43.0
Forearm length (mm)	38.8	37.4	30.0–40.0
Tail length (mm)	17.0	23.0	20.0–27.0
Ear length (mm)	8.0	8.0	9.0–12.0

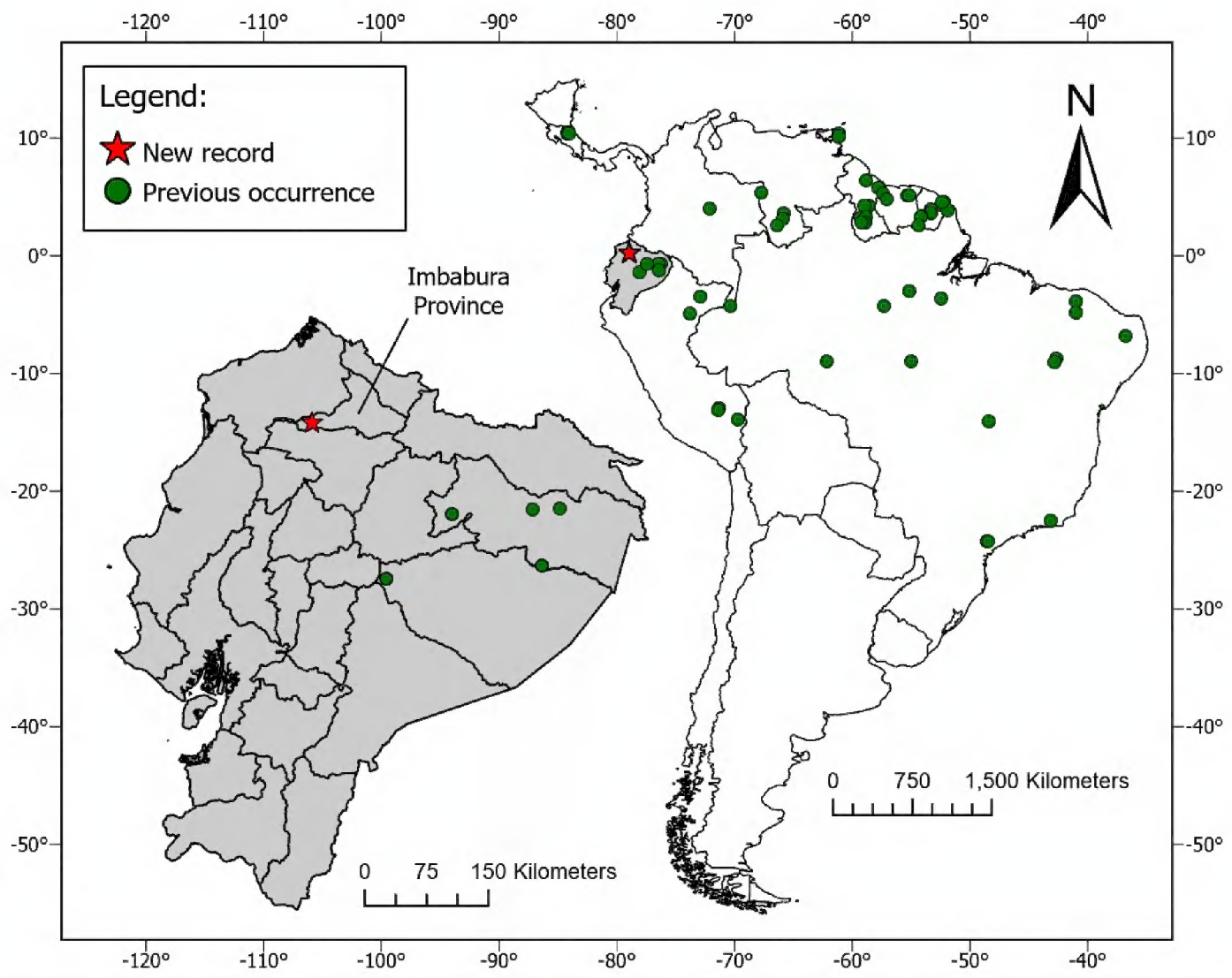

Figure 3. Records of *Furipterus horrens*, including occurrences previously recorded for Ecuador based on Albuja (1999), Reid et al. (2000), Tirira et al. (2020), and for the rest of its distribution retrieved from GBIF (2025).

DISCUSSION

Previously, the distribution of *Furipterus horrens* in Ecuador was thought to be limited to the Amazonian region (Albuja 1999; Reid et al. 2000; Tirira 2017; Tirira et al. 2020). Here, we show that the range of *F. horrens* extends to the Pacific slopes of the Andes, 290 km northwest of the nearest previous record (Figure 3). The discovery of *F. horrens* in Imbabura Province represents not just an increase in the geographical range of this taxon, but also the altitudinal range that it occupies. While past reports (Portella et al. 2017; Romero et al. 2022; Moras et al. 2024) mostly imply that *F. horrens* is confined to lowland ecosystems, this record demonstrates that *F. horrens* is capable of surviving at significantly higher, montane elevations.

Additionally, despite *Furipterus* currently being considered a monotypic genus, recent studies have proposed revisiting this taxonomy. Moras et al. (2024) have suggested that due to the patchy distribution of *F. horrens* across South and Central America, there is evidence for allopatric speciation within the genus. As such, these new and relatively isolated records of *F. horrens* in Ecuador are significant not just for the distribution of the genus, but potentially also its taxonomy. Genetic analysis with cyt-b shows a genetic distance of 10% between the specimen collected in the Manduriacu River Reserve (MECN 8160) and a specimen from Yasuní, Ecuador (AY621004), and a difference of 13.8% with individuals from Brazil (NC048476 and MK033190). This genetic divergence, also observed by Moras et al. (2024), is consistent in our analysis (Figure 2), and suggests that *F. horrens* comprises a species complex. High genetic divergence supports the Río Manduriacu Reserve population as a potentially undescribed species. However, it seems prudent to await additional material from western Ecuador to establish stable differences with the eastern lowland populations and to justify a taxonomic recognition.

Regardless, our findings demonstrate the need for further research into Chiropteran diversity in the northwest of Ecuador, a region that is notable for its high levels of species diversity and endemism. Like

much of the Neotropics, Chiroptera make up a significant proportion of the mammalian diversity, with recent studies documenting the presence of 182 species of bats in Ecuador (Tirira et al. 2024). However, habitat degradation due to agricultural monoculture and mining poses a serious and imminent threat to the bats of the region. As such, understanding the true extent of the chiropteran diversity present should be a research priority.

ACKNOWLEDGEMENTS

Special thanks go to Gabriel Alejandro for all his help in the field, and to Dario Armas, Jimmy Alvarez, and David Monteros, the rangers who assisted us. We thank Dr. Veronica Zamora-Gutierrez and Javier Robayo for their guidance and resources. Finally, we thank Dr. Ligiane Moras, Dr. Roberto Leonan M. Novaes, and an anonymous reviewer for providing valuable suggestions that improved the quality of the manuscript.

ADDITIONAL INFORMATION

Conflict of interest

The authors declare that no competing interests exist.

Ethical statement

No ethical statement is reported.

Funding

This study was financially supported by Fundación EcoMinga.

Author contributions

Conceptualization: IW, JB. Data curation: JB. Formal analysis: IW, LS. Funding acquisition: IW. Investigation: IW, JB. Methodology: IW, LS, JB. Visualization: IW. Writing – original draft: IW. Writing – review and editing: JB, LS.

Author ORCID iDs

Isabel Warren https://orcid.org/0009-0008-9501-8647
Laura Simba https://orcid.org/0009-0004-2442-7612
Jorge Brito https://orcid.org/0000-0002-3410-6669

Data availability

All data that support the findings of this study are available in the main text.

REFERENCES

Albuja L (1999) Murciélagos del Ecuador. 2nd ed. Cicetrónic Compañía Limitada, Quito, Ecuador, 175–178.

Alfaro-Lara H, Villalobos-Chaves D, Castillo-Gómez JI, Zuñiga-Montero AF, Pineda-Lizano W (2018) Rediscovery of *Furipterus horrens* (Chiroptera: Furipteridae) in Costa Rica. Mammalia 83: 352–356. https://doi.org/10.1515/mammalia-2018-006

Borisenko AV, Lim BK, Ivanova NV, Hanner RH, Hebert PDN (2008) DNA barcoding in surveys of small mammal communities: a field study in Suriname. Molecular Ecology Resources 8: 471–479. https://doi.org/10.1111/j.1471-8286.2007.01998.x

Clare EL, Lim BK, Fenton MB, Hebert PDN (2011) Neotropical bats: estimating species diversity with DNA barcodes. PLoS ONE 6. https://doi.org/10.1371/journal.pone.0022648

Clare EL, Lim BK, Engstrom MD, Egr JL, Hebert PDN (2007) DNA barcoding of neotropical bats: species identification and discovery within Guyana. Molecular Ecology Notes 7: 184–190. https://doi.org/10.1111/j.1471-8286.2006.01657.x

Dávalos LM (2005) Molecular phylogeny of funnel-eared bats (Chiroptera: Natalidae), with notes on biogeography and conservation. Molecular Phylogenetics and Evolution 37: 91–103. https://doi.org/10.1016/j.ympev.2005.04.024

Duda R, Dalapicolla J, Costa LP (2012) First record of the smoky bat *Furipterus horrens* (Cuvier, 1828) (Mammalia: Chiroptera) in the state of Espírito Santo, southeastern Brazil. Check List 8: 1362. https://doi.org/10.15560/8.6.1362

Emmons LH (1990) Neotropical rainforest mammals: a field guide. University of Chicago Press, Chicago, USA, 91 pp.

Gardner AL (2008) Family Furipteridae Gray, 1866. In: Mammals of South America. Volume 1: marsupials, xenarthrans, shrews, and bats. University of Chicago Press, Chicago, USA, 389–392.

GBIF (Global Biodiversity Information Facility) (2025) GBIF occurrence download. Global Biodiversity Information Facility, Copenhagen, Denmark. https://doi.org/10.15468/dl.hgvhze. Accessed on: 2025-2-4.

Ibáñez C (1986) Notes on *Amorphochilus schnablii* Peters, 1877 (Chiroptera, Furipteridae). Mammalia 49: 584–587.

Kimura M (1980) A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. Journal of Molecular Evolution 16: 111–120. https://doi.org/10.1007/bf01731581

Kumar S, Stecher G, Suleski M, Sanderford M, Sharma S, Tamura K (2024) MEGA12: Molecular Evolutionary Genetic Analysis version 12 for adaptive and green computing. Molecular Biology and Evolution 41: 1–9. https://doi.org/10.1093/molbev/msae263

Maddison WP, Maddison DR (2023) A modular system for evolutionary analysis. Version 3.81. The Mesquite Project, Santa Barbara, USA. http://www.mesquiteproject.org Accessed on: 2025-2-17.

Mammal Diversity Database (2024). Mammal Diversity Database (version 1.13). Zenodo, Brussels, Belgium. https://doi.org/10.5281/zenodo.10595931 Accessed on: 2025-2-17.

Mickleburgh SP, Hutson AM, Racey PA (2002) A review of the global conservation status of bats. Oryx 36: 18–34.

Molina M, Oliveira G, Oliveira RRM, Nunes GL, Pires ES, Prous X, Ribeiro M, Vasconcelos S (2024) Complete mitochondrial genomes of three vulnerable cave bat species and their phylogenetic relationships within the order Chiroptera. Bhardwaj P (Ed.). PLoS ONE 19: e0308741. https://doi.org/10.1371/journal.pone.0308741

Moras LM, Nobre CC, Vasconcelos S, Garbino GST, de Souza ÉMS, Santos FR, Oliveira G, Tavares V da C (2024) Almost two hundred years of monotypy and a poorly known life history: multiple lineages of *Furipterus* (Chiroptera: Furipteridae) were hidden by rocks. Mammalian Biology. https://doi.org/10.1007/s42991-024-00465-9

Myers N, Mittermeier RA, Mittermeier CG, da Fonseca GAB, Kent J (2000) Biodiversity hotspots for conservation priorities. Nature 403: 853–858.

Patterson B, Pascual R (1968) The fossil mammal fauna of South America. The Quarterly Review of Biology 43: 409–451. https://doi.org/10.1086/405916

Pavan AC, Martins FM, Morgante JS (2013) Evolutionary history of bulldog bats (genus *Noctilio*): recent diversification and the role of the Caribbean in Neotropical biogeography. Biological Journal of the Linnean Society, 108: 210–224. https://doi.org/10.1111/j.1095-8312.2012.01979.x

Portella TP, Kaku-Oliveira NY, Jennifer, Sessegolo GC (2017) First record of the vulnerable bat *Furipterus horrens* Cuvier, 1828 (Chiroptera: Furipteridae) in the state of Paraná, southern Brazil. Check List 13: 127–134. https://doi.org/10.15560/13.4.127

Reid F, Engstrom MD, Lim B (2000) Noteworthy records of bats from Ecuador. Acta Chiropterologica 2: 37–51.

Romero V, Vallejo A, Boada C (2022) Mamíferos del Ecuador: *Furipterus horrens*. Pontificia Universidad Católica del Ecuador, Quito, Ecuador. https://bioweb.bio/faunaweb/mammaliaweb/FichaEspecie/Furipterus%20horrens Accessed on: 2025-2-17.

Sahlin K, Lim MCW, Prost S (2021) NGSpeciesID: DNA barcode and amplicon consensus generation from long-read sequencing data. Ecology and Evolution 11: 1392–1398. https://doi.org/10.1002/ece3.7146

Sikes RS (2016) 2016 guidelines of the American Society of Mammalogists for the use of wild mammals in research and education. Journal of Mammalogy 97: 663–688. https://doi.org/10.1093/jmammal/gyw078

Tirira DG (2017) A field guide to the mammals of Ecuador. Editorial Murciélago Blanco, Quito, Ecuador, 401–404.

Tirira DG, Greeney HF, Omaca C, Baihua O, Killackey RP (2020) Species richness and ethnozoological annotations on mammals at the Boanamo indigenous community, Waorani territory, Orellana and Pastaza provinces, Ecuador. Mammalia 84: 535–551. https://doi.org/10.1515/mammalia-2019-0144

Tirira DG, Brito J, Burneo SF, Pinto CM, Salas JS (2024) Mammals of Ecuador: official updated species checklist. Asociación Ecuatoriana de Mastozoología, Quito, Ecuador, 39 pp.

Voigt CC, Kingston T (2015) Bats in the Anthropocene. In: Voigt CC, Kingston T (Eds.) Bats in the Anthropocene: conservation of bats in a changing world. Springer Online, Heidelberg, Germany, 1–9.

APPENDIX

Table A1. Specimens of the *Furipterus horrens* complex used in phylogenetic analyses.

Species	GenBank accession #		Locality	Source
	cyt-b	COI		
F. horrens	MK033190		Canaa dos Carajás, Brazil	Molina et al. 2024
F. horrens	NC048476		Carajás National Forest, Brazil	Molina et al. 2024
F. horrens	AY621004		Parque Nacional Yasuní, Ecuador	Dávalos 2005
F. horrens		JF448846	Parque Nacional Yasuní, Ecuador	Clare et al. 2011
F. horrens		JX989224	FLONA Río Preto, Brazil	Duda et al. 2012
F. horrens		EU096741	Sipaliwini, Surinam	Borisenko et al. 2008
F. horrens		JF459160	Forest Potaro-Siparuni, Guyana	Lim et al. 2012
F. horrens		EU096742	Sipaliwini, Surinam	Borisenko et al. 2008
F. horrens		EF080358	East Berbice- Corentyne, Guyana	Clare et al. 2007
F. horrens	PV147124	PV147227	Reserva Río Manduriacu, Ecuador	This study
Outgroup				
N. leporinus		JF455173	Takutu-Essequibo, Guyana	Clare et al. 2011
N. leporinus		JF455172	Takutu-Essequibo, Guyana	Clare et al. 2011
N. leporinus	JX257161		Takutu-Essequibo, Guyana	Pavan et al. 2013
N. leporinus	JX235630		Ji-Paraná, Rondônia, Brazil	Pavan et al. 2013